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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                           Result
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                                                                                                                                                                                                                                                                                              NO.
                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
1067.5
1067.5
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756
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Sp_archea:*

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Sp_fungi:*

Sp_fungi:*

Sp_funwan:*

Sp_muman:*

Sp_manmal:*

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Sp_page:*

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Match Length DB
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Gapop 10.0 , Gapext 0.5
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1654
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sp_phage:*
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sp_bacteria:*
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sp_unclassified:*
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8 0913R6
2 09RWH9
2 09K8H9
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           O9mba2 arabidopsis
O9fv40 tagetes ere
O9lwy6 oryza sativ
O9ty36 nephroselmi
O9ty37 deinococcus
O9rwb7 deinococcus
O9k8h9 bacillus ha
O67033 aquifex aeo
O9pdq8 xylella fas
O9hy26 pseudomonas
O9sp90 oryza sativ
O9kqn8 vibrio chol
O9dq96 neisseria m
O9ag19 neisseria m
O9ag19 neisseria g
O9v165 pyrococcus
O29868 methanobact
O58346 pyrococcus
O29562 archaeoglob
                                                                                                                                                                                                                                                                                             Description
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4 4 5	4 2 3	41	4 3 9 9	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
196 195	197 196.5	202	209.5	218	224	227	228	230	236	236.5	238	238.5	239.5	241	243.5	46	247.5	249	250	254	262.5	266
	11.9 11.9			13.2		•	13.8		14.3		14.4	14.4	14.5	14.6	14.7		15.0		15.1	15.4	15.9	
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Q9kt68 Q9x117	058711 Q9v0d9	Q9v0c7	083825 067267	Q9z5s7	Q9zm33	Q91b16	Q9kqd3	025678	087380	Q44757	Q9aen5	044911	Q56340	. Q9pj56	Q9hqy5	Q9ka54	Q9v1r2	Q9rge0	Q91775	059249	Q9hnf1	059470
vibrio chol thermotoga	pyrococcus pyrococcus	pyrococcus	treponema p	zymomonas m			vibrio chol	helicobacte	pseudomonas	borrelia bu	burkholderi		treponema p	campylobact	halobacteri	bacillus ha	pyrococcus	pseudomonas	xanthomonas	pyrococcus	halobacteri	pyrococcus

## ALIGNMENTS

Qy	wa Qu Qu	SQ	DR	DR	DR	RL R	D 70	RT	RA	RA	RX	<u>ج</u>	7 Z	Z I	R R	RA	RP	RN	o <b>x</b>	8	ဂ္ဂ	ဂ္ဂ	SO	G N	DE	DI	בן בן	7 7	ב ב	RESULT Q9MBA2
MASLRLFSTNHQSLLLPSSLSQKTLISSPRFVNNPSRRSPIRSVLQFNRKPELAGETPF	Query Match 100.0%; Score 1654; DB 10; Length 326; Best Local Similarity 100.0%; Pred. No. 2.1e-118; Matches 326; Conservative 0; Mismatches 0; Indels 0; Gaps	AA;	InterPtO; IPROUD/U/; ParA; Pfam; PFOC991; ParA; 1.	EMBL; AB009056; BAB08725.1;	EMBL; AB030278; BAA90261.1;	DNA Res. 5:41-54(1998).	Sequence features of the regions of 1,456,315 bp covered by nineteen	l analysis of Arabidopsis thaliana	ta s.	Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miya'ima N.,	MEDLINE=98290546; PubMed=9628582;	STRAIN-COLUMBIA;	SPOTENCE FROM N A		"Arabidopsis thaliana minD homolog involved in plastid division."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.	, Takahashi		(E)	NCBI_TaxID=3702;	eurosids II; Brassicales; Brassicaceae; Arabidopsis.	edons; core e	Eukarvota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;	Arabidopsis thaliana (Mouse-ear cress).	MIND.	M SITE-DETERMININ	(TrEMBLrel, 17, Last	01-00T-2000 (frembliet to to tector)	(Trampine) 15	Q9MBA2 PRELIMINARY; PRT; 325 AA.	

Q9SPP0 Q9KQN8 Q9JQY6 Q9AG19 Q9V165 Q9V165 027868 058346 029562

Q9UYS0

Q9uys0 pyrococcus

Qy

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01-MAR-2001
01-JUN-2001
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NCBI_TaxID=13708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-2000) to the EMBL; AF251019; AAG10431.1; InterPro; IPR000707; Para. Pfam; PF00991; Para; 1. SEQUENCE 295 AA; 32756 MW
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"Analysis of carotenoid biosynthetic
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                                                                                          FNRKPELAGETPRIVVITSGKGGVGKTTTTANVGLSLARYGFSVVAIDADLGLRNLDLLL 106
                                                                                                                                                                                                                 GLENRVNYTCVEVINGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDA 166
RDIKMIVNRVRTDLIRGEDMMSVLDVQEMLGLSLL----SDTRGFEVIRSTNRGFPLVLN
                      RDIKMIVNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPEDS---EVIRSTNRGFPLVLN 283
                                                                                                                                                                                          GLENRVNYTVVEVLNGDCRLDQALVRDKRWSNFELLCISKPRSKLPLGFGGKALVWL-DA
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32756 MW;
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RESULT
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                                             Q9T3P6
Q9T3P6;
01-MAY-2000
01-MAY-2000
01-JUN-2001
SEPTUM-SITE |
MIND.
Chloroplast.
Eukaryota; Viridiplantae; Chlorophyta; Prasinc Chlorodendrales; Chlorodendraceae; Nephroselmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6 clone:P0644B06.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases EMBL; AP001129; BAA90628.1;
InterPro; IPR000707; ParA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0T-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO CHLORELLA VULGARIS C-27 CHLOROPLAST DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9LWY6;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LWY6
                                   Nephroselmis olivacea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrhartoideae;
                                                                                                                                                                              291
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                                                                                                                                            4
                                                                                                                                                                                                   E--PKKR-GFFSFFGG
                                                                                                                                                                                                                                       EMLGLSLLGVIPEDSEVIRSTNRGFPLVLNKPPTLAGLAFEQAAWRLVEQDSMKAVMVEE
                                                                                                                                                                                                                                                                        TTTANVGLSLARYGFSVVAIDADLGLRNLDLLLGLENRVNYTCVEVINGDCRLDQALVRD 133
                                                                                                                                                                              QERPKKKAGFFSFFGG
                                                                                                                                                                                                                          EMLGLPLLGVVPEDAEVIRSTNRGVPLVLNDPPTPAGLALEQATWRLVERDAMTAVMVEE
                                                                                                                                                                                                                                                                                                                       RALHDLQLLCLSKPRSKLPLAFGSKTLTWVADALR-RAANPPAFILIDCPAGVDAGFVTA
                                                                                                                                                                                                                                                                                                                                   KRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTRPEGSPDFIIIDCPAGIDAGFITA 193
                                                                                                                                                                                                                                                                                                                                                                    TTTANLAASLARLSLSAVAVDADAGLRNLDLLLGLENRVHLTAADVLAGDCRLDQALVRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                216;
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                                                                    (TrEMBLrel.) (TrEMBLrel. (TrEMBLrel.
                                                         DETERMINING
                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   ---RCPPPASSPARHGG-----RTAPELSGPTPRVVVVTSGKGGVGKT
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32341 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.5%;
68.4%;
                                                                                                                                                                              306
                                                         13, Created)
13, Last sequence update)
17, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1067.5; Db L., Pred. No. 1.1e-73;
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CECAB38219512690 CRC64;
                                                                                                                    274
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  Prasinophyceae;
nroselmis.
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                                                                    update)
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RESULT
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Best Local
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases EMBL; AJ245645; CAB53105.1; -.
InterPro: IPR000707; ParA.
Pfam; PF00991; ParA; 1.
Cell division; Chloroplast.
SEQUENCE 359 AA; 40804 MW; E550EAF50BC0A51E CRC64;
                                                                                                                                                                                       Chloroplast.

Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Prototheca.
                                                                                              Knauf U., Hachtel W.;

"A 22 kb fragment of the 53 kb plastid genome of the colourless algaerototheka wickerhamii containing atp-, rpl-,rps-, rrn-, and trn-
                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CELL DIVISION INHIBITOR MIND.
                                                                                                                                                      STRAIN-263-
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Q9TJR6;
                                                                                                                                                                                                                                                       Prototheca wickerhamii.
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF137379; AAD54908.1; -.
EMBL; AF137379; AAD54881.1; -.
InterPro; IPR000707; ParA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-99396694; PubMed-10468594; Turmel M., Otis C., Lemieux C.; "The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: Insights into the architecture of ancestral chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                     249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 LIDCPAGIDAGFVNAIAPADEAILVTTPEITAIRDADRVAGLLEANDFYNVRLVANRVRP 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVIVITSGKGGVGKTTATANLGMCIARLGYRVALIDADIGLRNLDLLLGLENRVVYTAME 73
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58.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        radiodurans R1.";
Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White O., Eisen J.A., Heidelberg J.E., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9RWB7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence of the control of the co
119 VINGDÇRLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTR------ 170
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000392; NitrogenaseII
InterPro; IPR00707; ParA.
Pfam; PF00142; fer4_NifH; 1.
Pfam; PF00991; ParA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001931; AAF10331.1; TIGR; DR0752; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20036896; PubMed=10567266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the radioresistant bacterium Deinococcus
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                                                                                                            12 KVIVVTSGKGGVGKTTTTANIGAALARLGEKVVVIDVDVGLRNLDVVMGLESRVVFDLVD 71
                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 LSLLGVIPEDSEVIRSTNRGFPLVLNKPPTLAGLAFEQAAWRLVEQD 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159;
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                               29420 MW;
                                                                                                                                                                                                                               34.7%; Score 573.5; DB 2
44.3%; Pred. No. 4.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17, Last annotation update) PROTEIN.
                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
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Pred. No. 1.6e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                               AD74FDCF45820D0C CRC64;
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
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                                                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                    Length 276;
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                                                                                                                                                                                              Gaps
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SEPTUM SITE-DETERMINING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     halodurans and genomic sequence comparison with Bacillus Subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
EMBL; APO01517; BAB66746.1; -.
InterPro; IPR000392; NitrogenaseII.
InterPro; IPR000707; ParA.
Pfam; PF00142; fer4_NifH; 1.
Pfam; PF00142; fer4_NifH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Staphylococcus group; NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRĀIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
MEDLINE-20512582; PubMed-11058132;
MEDLINE-20512582; PubMed-11058132;
MEDLINE-20512582; MEDLINE R., Macamura Y., Ogasawara N., Kuhara
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=C-125 / JCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus halodurans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 AGDAFMATAQRIQGQDVPFPKLTEEE---KGIWAAIRRLFGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRLVVNRLRPKMVASGNMLSIDDMVDILGVKPIGIVPEDEGIIVSTNVGEPAVLGK--TK
                                                                                                                                                                                                                              IKGEDMMSVLDVQEMLGLSLLGVIPEDSEVIRSTNRGFPLVLNKPPTLAGLAFEQAAWRL 300
                                                                                                                                                                                                                                                                                                                                                    DCPAGIDAGFITAITPANEAVLVTTPDITALRDADRVTGLLECDGIRDIKMIVNRVRTDM
                                                                                                                                                                                                                                                                                                                                                                                                                               EGRCRLKQALIKDKRFECLNLLPAAQTKDK--SAVTPEQMKEIVEELKQ----EYDYVLI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVITSGKGGVGKTTTSANIGTALALSGKKVCLVDTDIGLRNLDVVMGLENRIIYDLVDVV 64
                                                                                                                                       VEODSMKAVMVEEEPKKRGFFSFFG
                                                                                                                                                                                                MKNGEMLDVDEIVSILAIELLGIVVDDENVIKFSNKGEPIALH-PDSKASVAYRNIARRI
                                                                                                                                                                                                                                                                                                                DCPAGIEQGFKNAVAGADKAIVVTTPEISSVRDADRIIGLLEKEEVEAPRLVVNRIRGHM
                                                                                    LGETVPLMSFEQEKGVLAKIKSFFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28818 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.4%;
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Pred. No. 2.9e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
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01-AUG-1998 (TrEMBLrel. 0
01-AUG-1998 (TrEMBLrel. 0
01-JUN-2001 (TrEMBLrel. 1
SEPTUM SITE-DETERMINING P
MIND2 OR AQ_877.
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        067033
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                                                                                                                                                                                                                                                                                                                                                                Q9PDQ8;
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InterPro: IPR000707; ParA.
Pfam: PF00142; fer4_NifH; 1.
Pfam: PF00991; ParA; 1.
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EMBL; AE000712; AAC06996.1;
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                                                                                                                                                                                                                                                         01-00T-2000 (TremBLrel. 15, Created)
01-0CT-2000 (TremBLrel. 15, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation updat
SEPTUM SITE-DETERMINING PROTEIN.
MEDLINE=20365717; PubMed=10910347; Simpson A.J.G., Reinach F.C., Arru
                                                STRAIN=9A5C;
                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                        Xylella fastidiosa
                                                                                                                                                                                                                                      XF1321
                                                                                                                            NCBI_TaxID=2371;
                                                                                                                                                          Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 IDCPAGIDAGFITAITPANEAVLYTTPDITALRDADRYTGLLECDGIRDIKMIVNRVRTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 MVKRGAMLSVEDIVDILKAEIIGIIPBEPKLVDFTNRGEPIVLDEKFPASQAII-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 LEGRVPYEKALVKDKRGLSLWLLPANQRANKDVIDIE----KWNKTVEEIKNSGNYDYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 IVVITSGKGGVGKTTTTANVGLSLARYGFSVVAIDADLGLRNLDLLLGLENRVNYTCVEV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WRLVEQDSMKAVMVEEEPKKR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTRPEGSPDFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIKGEDMMSVLDVQEMLGLSLLGVIPEDSEVIRSTNRGFPLVLNK--PPTLAGLAFEQAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDSPAGIEKGFQIAVSPADKALIVVNPEVSSIRDADRVIGLLESMDKRNYKVIVNRIKWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108;
                                                                                                                                                                                Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTARRLMGESIPLKR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aquificaceae;
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07, Last sequence update)
17, Last annotation update)
PROTEIN MIND.
                                                                                                                                                                                  gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 516; DB 2; Length 262; pred. No. 1.1e-31; 5; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
     Arruda P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535C2E5F3D5B352A CRC64;
                                                                                                                                                                                     subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aquifex
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                                                                                                                                                                                                                                                                                                                                                                                                   269
                                                                                                                                                                                                                                                                                                                                                                                                   ĀĀ
        Abreu F.A.,
                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                        Xanthomonas group;
        Acencio
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          :3
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RESULT
Q9HYZ6
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OCCUPEDDAN
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                                                                                                             Q9HYZ6
Q9HYZ6
Q9HYZ6
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CELL DIVISION INHIBITOR MIND.
MIND OR PA3244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrígues V., de Rosa A.J.M., de Rosa V., de Rosa A.J.M., de Rosa V., Sawasaki H.E., da Silva F.R., Silva W.A. Jr., da Silva F.R., Silva W.A. Jr., da Silva F.R., Silva W.A. Jr., de Souza A.A., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meddanis J., Setubal J.C.;
"The genome sequence of the plant pathogen Xylella fastidiosa."; RMBL, AE00395; AAF84130.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00142; fer4_NifH; 1. Pfam; PF00991; ParA; 1.
                                         Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                   Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome
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InterPro; IPR000707; ParA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 FEQAAWRLVEQD-SMKAVMVEEEPKKRGFFS-FFGG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 CDSPAGIEKGASLAMYFADRAVVVVNPEVSSVRDSDRIIGLLDSKTKKAETGGSIITTLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 IDCPAGIDAGFITAITPANEAVLVTTPDITALRDADRVTGLL-----ECDGIRDIKMI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 IIVITSGKGGVGKTTTSASLACGLARRGKKVVVIDFDVGLRNLDLIMGCERRVVYDFVNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEDAVGRILGEDHPMRFTTVE----KKGFFSKLFGG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPEDSEVIRSTNRGFPLVLNKPPTLAGLA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDGEATLKQALIKDKRFDNLYLLAAAQTRDKDALTKEG - - VEKVLNELQA - - EGF - DYIC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTRYSPARVESGEMLSIADVEEVLGLKAIGVIPESGDVLNASNKGEPVILDN-NSLAGLA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTRPEGSPDFII 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 1.4e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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Query Match
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunityic pathogen.", Nature 4061959-964(2000), Paulsen I.T., Paulsen I.T., Pam., PSEMEL, AE004747 1, AAG06632.1; -. InterPro; JPR000707; Para.
                                                                                                                                                STRAIN-CV. IR-BB21;
Han F., Kilian A., Chen J.P., Kudrna D., Steffenson B., Yamamoto K.,
Matsumoto T., Sasaki T., Kleinhofs A.;
"Sequence analysis of a rice BAC covering the syntenous barley Rpg1
                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 271 AA;
SEQUENCE
                                   Pfam; PF00142; fer4_NifH; 1. Cell division.
                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                 CELL DIVISION INHIBITOR MIND HOMOLOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9SPP0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9SPP0
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                                                                                                                 Genome 0:0-0(1999)
                                                                                                                                                                                                                             SEQUENCE FROM N.A
                  NON_TER
                                                                                            EMBL; AF149810;
                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 LRKDFDXIICDSPAGIEKGAHLAMYFADEAIVVTNPEVSSVRDSDRWLGLLASKSQRAEK 168
                                                                           nterPro; IPR000392; NitrogenaseII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 NKPPTLAGLAFEQAAWRLVEQDSMKAVMVEEEPKKRGFFS-FFGG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 -----MIVNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPEDSEVIRSTNRGFPLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 GSPDF ~ - IIIDCPAGIDAGFITAITPANEAVLVTTPDITALRDADRVTGLLECDGIRDIK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 VINGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDAL------KTRPE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 DEQSD-AGQAYSDAVDRLLGKEIPHRFL---DVQKKGFLQRLFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 VVNGEATLTQALIKDKRLENLHVLAASQTRDK------DALTKEGVEKVMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 RIVVITSGKGGVGKTTTTANVGLSLARYGFSVVAIDADLGLRNLDLLLGLENRVNYTCVE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KILVVTSGKGGVGKTTTSAAIGTGLALRGFKTVIVDFDVGLRNLDLIMGCERRVVYDFVN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEEPIKEHLLITRYNPERVTKGEMLGVDDVEEILAIRLLGVIPESQAVLKASNQGVPVIL
179 AA;
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                  179
                                                                                            AAF00142.1;
                    179
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18705 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.1%; Score 480.5; DB 2
39.6%; Pred. No. 5.6e-29;
tive 54; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0367E2BC42A06444 CRC64;
  3DE6FAF7DAE76E77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 AA
                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta; a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 271;
                                                                                                                                                                                                                                                                                                                                                                                    update)
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Best Local Similarity
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9KQN8;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN=EL TOR N16961 / SEROTYPE 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                           cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9KQN8
                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE004271; AAF95108.1; TIGR; VC1960; -.
                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                InterPro;
184 LLLTRYNPARVTQGEMLSVQDVEEILHVPLLGVIPESQAVLNASNKGVPVIFDDQSD-AG
                                                             124
                                                                                          179
                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 KRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTRPEGSPDFIIIDCPAGIDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence of both chromosomes
                                                                                                                                                                                                              59
                                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
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                                                                                                                                                                                                RIVVITSGKGGVGKTTTTANVGLSLARYGFSVVAIDADLGLRNLDLLLGLENRVNYTCVE 118
                             MIVNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPEDSEVIRSTNRGFPLVLNKPPTLAG
                                                                         TIDCPAGIDAGFITAITPANEAVLVTTPDITALRDADRVTGLLECDGIR-----DIK--
                                                                                                                     VINGEATLNQALIKDKRNENLFILPASQTRDKDALTKDG---VQRVLNDLK---
                                                                                                                                                 VINGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTRPEGSPDFI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTANVGLSLARYGFSVVAIDADLGLRNLDLLLGLENRVNYTCVEVINGDCRLDQALVRD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLPS-----RCPPPASSPARHGG-----RTAPELSGPTPRVVVVTSGKGGVGKT 51
                                                         ICDSPAGIEQGALMALYYADEAIVTINPEVSSVRDSDRILGILDSKSMRAEQGQAPIKQH
                                                                                                                                                                               RIIVVTSGKGGVGKTTSSAAIASGLALRGKKTAVIDFDIGLRNLDLIMGCERRVVYDFVN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTANLAASLARLSLSAVAVDADAGLRNLDLLLGLENRVHLTAADVLAGDCRLDQALVRH 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100;
                                                                                                                                                                                                                                                                                                                                                PF00991; ParA;
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SITE-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria;
                                                                                                                                                                                                                                                                                                                      276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
-DETERMINING PROTEIN MIND.
                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                            57; Mismatches
                                                                                                                                                                                                                                                         Score 468; DB 2;
Pred. No. 5.2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 479; DB 10;
Pred. No. 4.1e-29;
                                                                                                                                                                                                                                                                                                                    46CB44013A847F59 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     of the cholera pathogen Vibrio
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                                                                                                                                                                                                                                                                       Length 276,
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Best Local
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01-OCT-2000
01-OCT-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., KetChum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:1809-1815(2000).

EMBL; AL162752; CAB83415.1;

EMBL; AE002374; AAF40628.1;

TIGR; NMB0171; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MC58 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis (serogroup A), and Neisseria meningitidis (serogroup B). Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIND OR NMA0100 OR NMB0171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00991; ParA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=65699, 491;
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                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                          3 KIIVVTSGKGGVGKTTTSASIATGLALRGYKTAVIDFDVGLRNLDLIMGCERRVVYDLIN 62
                                                                                                                                                                                                                                                                                                                                          VIQGEATINGALIKOKNCENLFILPASQTROKDALTREG--VEKVMQELSGKKMGF-EYI 119
IVNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPEDSEVIRSTNRGFPLVLNKPPTLAGL
                                                                                                                                                                                                                                             VINGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTRPEGSPDFI 178
                                                         ICDSPAGIEQGALMALYFADEAIVTTNPEVSSVRDSDRILGILQSKSHKAEQGGSVKEHL
                                                                                                                      IIDCPAGIDAGFITAITPANEAVLVTTPDITALRDADRVTGLL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29559 MW;
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15, Last sequence update)
17, Last annotation update
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                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 449.5; DB 2
Pred. No. 1.3e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9ACDB52A03BD6170 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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Best Local
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Microbiology 147:225-237(2001).
EMBL; AF345908; AAK30126.1; -.
SEQUENCE 271 AA; 29597 MW; 87EC6FE31067B542 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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SEQUENCE FROM N.A. STRAIN-ORSAY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ramirez-Arcos S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=485;
                                             Archaea; Euryarchaeota;
NCBI_TaxID=29292;
                                                                                                                                                                          Q9V165;
                                                                                                                                                                                              Q9V165
                                                                              Pyrococcus abyssi.
                                                                                               PAB1983
                                                                                                               CELL DIVISION INHIBITOR (MIND-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 LITRYSPERVAKGEMLSVQDICDILHIPLLGVIPESQNVLQASNSGEP-VIHQDSVAASE 238
                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 AYKDVIARLLGENREMRFL----EAEKKSFFKRLFGG 271
                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 VINGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTRPEGSPDFI 178
                                                                                                                                                                                                                                                                          239
                                                                                                                                                                                                                                                                                                        292 AFEQAAWRLY-EQDSMKAVMVEEEPKKRGFFS-FFGG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 VIQGEATLNQALIKDKNCENLFILPASQTRDKDALTREG--VEKVMQELSGKKMGF-EYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KIIVVTSGKGGVGKTTTSASIATGLALRGYKTAVIDFDVGLRNLDLIMGCERRVVYDLIN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIVVITSGKGGVGKTTTTANVGLSLARYGFSVVAIDADLGLRNLDLLLGLENRVNYTCVE 118
                                                                                                                                                                                                                                                                                                                                         LITRYSPERVAKGEMLSVQDICDILRIPLLGVIPESQNVLQASNSGEP-VIHQDSVAASE
                                                                                                                                                                                                                                                                                                                                                                        IVNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPEDSEVIRSTNRGFPLVLNKPPTLAGL 291
                                                                                                                                                                                                                                                                                                                                                                                                      ICDSPAGIEQGALMALYFADEAIVTTNPEVSSVRDSDRILGILQSKSRKAEQGGSVKEHL 179
                                                                                                                                                                                                                                                                          AYKDVIARLLGENREMRFL----EAEKKSFFKRLFGG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                     IIDCPAGIDAGFITAITPANEAVLVTTPDITALRDADRVTGLL-----ECDGIRDIKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Szeto J., Beveridge T., Victor C., Francis F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11160816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.2%; Score 449.5; DB 2
37.5%; Pred. No. 1.3e-26;
tive 63; Mismatches 93
                                                                Thermococcales; Thermococcaceae; Pyrococcus
                                                                                                                                                                                              260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 AA
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InterPro; [PR000707; ParA.
Pfam; PF00142; fer4_NifH; 1.
Pfam; PF00991; ParA; 1.
Cell division; Complete proteome.
SEQUENCE 260 AA; 27657 MW; 8C0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."; substitute (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AJ248284: CAB49485.1; -. ___
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heilig R.;
                                                                                                                                                                                                                                                                                    119 VINGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGF----GGKALEWLVDALKTRPEG- 173
221 PAAIAYKEIAAKLAGIKWKPPEPES------PVKRIFRALFGG 257
                                                                                                                                                            105 IREISQMGDFILIDAPAGLELTSITALLIGKELIIVTNPEIAAITDSLKTKLVAEKLGTL 164
                                                                                                                                                                                                  174 -----SPDFIIIDCPAGIDAGFITAITPANEAVLYTTPDITALRDADRYTGLLECDGIR 227
                                       288 LAGLAFEQAA-----WRLVEQDSMKAVMVEEEPKKRGFFSFFGG 326
                                                                                                                                                                                                                                            63 VLAGEADLKDAIYEG-------PAGVKVIPGGLSLEKIKKARAERLRDL 104
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                            4 RSIVFASGKGGTGKTTTVANIGVALAQFGKDVILIDADITMANLSLILGMED-IPVTLHD 62
                                                                                                          DIKMIVNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPEDSEVIRSTNRGFPLVLNKPPT 287
                                                                               PLGAILNRVTSEKTE----LSREEIEALLEVPVLGTVPEDPEVKRASAYGVPLVVKNPTS
                                                                                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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AA; 27657 MW; 8C02C95C720A35B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               22.1%; score 366; DB 1; Length 260; 32.9%; Pred. No. 2.9e-20;
                                                                                                                                                                                                                                                                                                                                                                                                           54; Mismatches
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7;

Search completed: February 11, 2002, 13:32:41 Job time: 88 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Database
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Maximum DB seq length: 2000000000
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                  February 11, 2002, 13:31:13; Search time 24.36 Seconds (without alignments) 991.293 Million cell updates/sec
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Listing first 45 summaries
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1654
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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198	206	209	224	224	888	888	1648	1648	1654	1654	Score	
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412	388	425	297	294	174	174	344	326	343	326	Query: Match Length	
18	21	18	18	19	21	21	21	21	21	21	DB	
AAW20443	AAB11657	AAW21013	AAW20738	AAY10990	AAG46532	AAG12923	AAG12921	AAG12922	AAG46530	AAG46531	ID	SUMMARIES
H. pylori čytoplas		г.		æ			Arabidopsis thalia	•		Arabidopsis thalia	Description	

thal	AAG11243	21	223	7.1	117	45
ŝ	AAG43416	21	222	7.1	117	44
al	AAG11244	21	222	7.1	117	43
HTRM clone 1870914	AAY73353	21	292	•	118	42
ğ	AAG91316	22	261	•	118	41
1 fre	AAW89905	20	243	•	N	40
Expressed antigen	AAW90006	20	242	•	120.5	39
Expressed antiqen	AAW90007	20	196	•	N	38
Protein which is s	AAY37626	20	317	•	121	37
Chlamydia pneumoni	AAY35442	20	255	7.6	125	36
EpsB. Lactococcus	AAB47419	22	231	•	N	3 5
ps2C protein	AAY68955	21	225	•	128.5	34
reptococcus pne	AAY81771	21	227	•	141	33
cytopl	AAW20504	18	171	•	145	32
is thal	AAG41435	21	296	•	(n	31
Arabidopsis thalia	AAG41434	21	350	•	154.5	30
menir	AAY75107	21	257	•	C.D.	29
mе	AAY75106	21	257	•	ĹЛ	28
is the	AAG22282	21	548	•	161	27
is th	AAG39875	21	547	•	161	26
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is th	AAG22283	21	532	•	161	24
5	AAG39877	21	400	•	161	23
is thali	AAG22284	21	400	9.7	161	22
tamicum	AAG90129	22	478	•	164.5	21
ORFX ORF157	AAB40393	21	115	•	165	20
uman protein seq	AAB92570	22	271	0	171.5	19
glutamicum pr	AAG90990	22	375	0	~	18
t and ovar	AAB59022	21	288	0	176	. 17
in se	AAB94219	22	289		178	16
thal	AAG43414	21	313	۲	183	15
ali	AAG11242	21	313		183	14
ycobacterium tub	AAG81141	22	390	11.5	190	13
C qlutamicum prote	AAG93171	22	279	Ë	197.5	12

## ALIGNMENTS

RESULT AAG46531 25-FEB-1999 05-MAR-1999 09-MAR-1999 23-MAR-1999 25-MAR-1999 29-MAR-1999 01-APR-1999 06-APR-1999 16-APR-1999 16-APR-1999 AAG46531 standard; Protein; 326 AA. 06-SEP-2000 EP1033405-A2. Arabidopsis thaliana. Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; Arabidopsis thaliana protein fragment SEQ ID NO: 58550. 16-OCT-2000 (first entry) AAG46531; 25-FEB-2000; termination sequence. 2000EP-0301439 99US-0121825 99US-0123180 99US-012548 99US-0125788 99US-0125778 99US-0126785 99US-0126785 99US-0126785 99US-0126785 99US-0126785 99US-0126785

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Best Local
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28-OCT-1999;
29-OCT-1999;
                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
    25-FEB-2000; 2000EP-0301439.
                                                          EP1033405-A2
                                                                                   Arabidopsis thaliana.
                                                                                                                termination sequence.
                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 58549.
                                                                                                                                                                                                18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                     AAG46530 standard; Protein; 343 AA
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99US-0160768
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Pred. No. 4.8e-174;
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    20-MAY-1999
21-MAY-1999
24-MAY-1999
25-MAY-1999
27-MAY-1999
28-MAY-1999
01-JUN-1999
04-JUN-1999
07-JUN-1999
07-JUN-1999
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05-MAR 1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
06-APR-1999
16-APR-1999
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18-JUN-1999
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04-MAY-1999;
05-MAY-1999;
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07-MAY-1999;
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16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
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14-MAY-1999;
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14-MAY-1999;
990S 0132486

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promoter;
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25-FEB 1999
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29-OCT-1999;
                                            Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life
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secreted protein; cellular protein.
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06-DEC-1996;
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 Sequence
                                  cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                     Claims 27, 31; Page 195; 279pp; English.
                                                                                                                                                                                                                                                                                   products for the detection, prevention and treatment of H. pylori
                                                                                                                                                                                                                                                                                                     Helicobacter pylori nucleic acids and proteins - used to develop
                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-271811/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 stnrgfplvlnkpptlaglafeqaawrlveqdsmkavmveeepkkrgffsffgg 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 DADRVTGLLECDGIRDIKMIVNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPEDSEVIR 272
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 294 AA;
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96US-0759739.
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99US-0162142.
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The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
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                                                                                                                                                               The present sequence is a Helicobacter pylori cytoplasmic protein The protein may be used in a vaccine to prevent or treat H. pylor
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07-JUN-1995;
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                                                                                                                                                                                                                          Claim 61; Page 1154; 1481pp; English.
                                                                                                                                                                                                                                                                                                       Helicobacter pylori nucleic acid sequences and related
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                                                                                                                                                                                                                                                              infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                      polypeptide(s
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AB.
                                                                                                                                                                                                                                                                                                                                                                                                        Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0630405
95US-0487032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US09122
                                                                                                                                                                                                                                                                                      useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.5%; Score 224; DB 19; 29.1%; Pred. No. 4.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                        Mellgaerd BL;
                                                                                                                                                                                                                                                                                    for vaccines to treat or prevent H. pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06cp20302orf8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 294;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                            Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or previnfection, and to detect Helicobacter
The present sequence is a Helicobacter pylori cytoplasmic The protein may be used in a vaccine to prevent or treat F
                                                                                                                                        WPI; 1997-052306/05.
N-PSDB; AAT68266.
                                                                                                                                                                                                                                              01-APR-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
                                            Claim 61; Page 1402-1403; 1481pp; English.
                                                                                                                                                                                     Berglindh OT,
                                                                                                                                                                                                                   (ASTR ) ASTRA
                                                                                                                                                                                                                                                                                          06-JUN-1996;
                                                                                                                                                                                                                                                                                                                          19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                         WO9640893-A1
                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                duodenal ulcer disease; chronic gastritis; diagnosis; envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori cytoplasmic protein, hp5e15211orf13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW21013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW21013 standard; protein; 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 nssllkryvrerkilrkiapndlfsqsidqiasllvskletgtl----eipkeglksff 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acikinsknkdelflianmvaqpkegratyerlfkvaknnias-----lelhylgaie 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DALKTRPEG----SPDFIIIDCPAGIDAGFITAITPANEAVLYTTPDITALRDADRYTGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GETPRIVVITSGKGGVGKTTTTANVGLSLARYGFSVVAIDADLGLRNLDLLLLGLENRVNY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDSEVIRSTNRGFPLVLNKPPTLAGLAFEQAAWRLVEQDSMKAVMVEEEPKKRGFFSFF 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECDGIR-----DIKMIVNRV------RTDMIKGEDMMSVLDVQEMLGLSLLGVIP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ilhalkgeaklq----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCVEVINGDCRLDQALVRDKRWSNFELLCISKPRSKLPMG------FGGKALEWLV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d-----eegvlssldyividtgagigattqaflnasdcvvivttpdpsaitda-----y 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gnt-kfiaitsgkggvgksnisanlayslykkgykvgvfdadiglanldvifgvkthkn-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.5%; Score 224; DB 18; ilarity 29.1%; Pred. No. 4.5e-16; Conservative 40; Mismatches 106;
                                                                                                                                                                                                                   AΒ
                                                                                                                                                                                     Smith D,
                                                                                                                                                                                                                                              96US-0630405
95US-0487032
                                                                                                                                                                                                                                                                                            96WO-US09122.
                                                                                                                                                                                     Mellgaerd
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                                                                                                                                                                                     ВL
                                                                                         to treat or prevent H. pylori
   prevent or treat H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
               protein
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   pylori
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                Burr TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                    stress resistance; transgenic plant.
                                                                                                                                                                                                                                                                 Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer;
                                                                                                                                                                                                                                                                                                                     A. vitis hypersensitive response elicitor protein,
                                                                                                                                                                                                                                                                                                                                                                                                                            AAB11657 standard; Protein; 388
                                              (CORR ) CORNELL RES FOUND INC
                                                                               06-NOV-1998;
                                                                                                                   05-NOV-1999;
                                                                                                                                                   18-MAY-2000
                                                                                                                                                                                     WO200028056-A2
                                                                                                                                                                                                                      Agrobacterium vitis.
                                                                                                                                                                                                                                                                                                                                                       23-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 lhipiagivenmgsfvcehck-----keseifgsnsmsgl--leayntqilaklpl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 INGDCRLD---QALVRDKRWSNFELLCISKPRSKLPMGF----GGKALEWLVDALKTRPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 epkvrlggdkgepivishptsvsakifekma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 DSEVIRSTNRGFPLVLNKPPTLAGLAFEQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 mlsdiiwgdldvlvvdmppgtgdaqltlaqavplsagitvttpqivslddakrsldmfkk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 vvmissgkggvgksttsvnlsialanlngkvglldadvygpniprmmglq------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 sseetsailreniskamqekgvkalnldiktpp-----kpqapkpttknlaknikh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 IVVITSGKGGVGKTTTTANVGLSLARYGFSVVAIDADLGLRNLDLLLGLENRVNYTCVEV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VTGLLE-----CDGIRDIKMIVNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -nadvimdpsgkkliplkafg------vsvmsmgllydegqsliwrgpmlmraieq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STNHQSLLLPSSLSQKTLISSPRFVNNPSRRSPIRSVLQFNRKPE------LAGETPR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
            Herlache TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                98US-0107387.
                                                                                                                 99WO-US26079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.6%; Score 209; DB 18; 24.2%; Pred. No. 3.6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                             AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 425;
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                                                                                                                                                                                                                                                                                                                       NO:37.
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Zhang H;

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CC vitis HR elicitor proteins. The HR is a rapid, localised necrosis that

CC is associated with the active defence of plants against many pathogens,

CC and occurs when a pathogenic organism interacts with a nonhost plant

CC (i.e. one in which intracellular bacterial growth and disease development

CC (i.e. one in which intracellular bacterial growth and disease development

CC (i.e. one in which intracellular bacterial growth and disease development

CC (i.e. one in which intracellular bacterial growth and disease development

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      X S X E X E X X X
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AAW20443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAB11630-B11688 represent proteins from Agrobacterium vitis which elicit a hypersensitivity response (HR) in a plant. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 112-113; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a hypersensitive response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA61510.
Cytoplasmic; vaccine; prevention; treatment;
                                                            H. pylori cytoplasmic protein, 35163962.aa.
                                                                                                                         14-JUL-1997 (first entry)
                                                                                                                                                                                                                                                      AAW20443 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or polluting chemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 ilavasgkggvgksttavnlalallanglkvgildadvygpsmprllgisgrpg----- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 INGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGF---GGKALEW------LVDALK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 evawgeldvlvvdmppgtgdaqltmaqqvplsgavivstpqdlalidarkginmfkkvev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 TRPEGSPDFIIIDCPAGIDAGFITAI--TPANEAVLVTTPDITALRDADRVTGLLECDGI 226
                                                                                                                                                                                                                                                                                                                                                                                                           343 hsdagtpvvvsepespqalvyreiatrvwreverhstr 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 RDIKMIVNR-----VRTDMI-----KGEDMMSVLDVQEMLGLSLLGVIPEDSEVIR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 STNRGFPLVLNKPPTLAGLAFEQAA---WRLVEQDSMK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 pvlgvlenmsyfiapdtgarydifghggakae-----aeaigapflgevpltisire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 IVVITSGKGGVGKTTTTANVGLSLARYGFSVVAIDADLGLRNLDLLLGLENRVNYTCVEV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----gidgrii--vpmenyglkams----igflvdegtamiwrgpmvqsalmqmlr 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                      protein; 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.5%; Score 206; DB 21; Length 388; 25.9%; Pred. No. 6.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Mismatches 100;
   infection; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a Helicobacter pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-052306/05.
N-PSDB; AAT67616.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1996;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                         173
                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 -nadvimdpsgkkliplkafg------vsvmsmgllydeggsliwrgpmlmraieg 241
351 epkvrlggdkgepivishptsvsakifekma 381
                                                                                                                                                   302 lhipiagivenmgsfvcehck-----keseifgsnsmsgl--leayntqllaklpl 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 INGDCRLD---QALVRDKRWSNFELLCISKPRSKLPMGF---GGKALEWLVDALKTRPE- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 vvmissgkggvgksttsvnlsialanlngkvglldadvygpniprmmglq----- 192
                                                                                                                                                                                                                             217 ----VTGLLE-----CDGIRDIKMIVNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPE 266
                                                                                                                                                                                                                                                                                                   242 mlsdiiwgdldvlvvdmpprnrrcaahaaqavplsagitvttpqivslddakrsldmfkk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 sseetsailreniskamqekgvkalnldiktpp-----kpqapkpttknlaknikh 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 STNHQSLLLPSSLSQKTLISSPRFVNNPSRRSPIRSVLQFNRKPE-----LAGETPR 59
                                                                              DSEVIRSTNRGFPLVLNKPPTLAGLAFEQAA 297
                                                                                                                                                                                                                                                                                                                                                                                     -----GSPDFIIIDCPAGID--AGFITAITPANEAVLVTTPDITALRDADR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 AA;
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95US-0487032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.0%; Score 198; DB 18; Length 412; 23.9%; Pred. No. 5.7e-13;
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                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly I-lysine. The present sequence is a protein described in the avament figures.
                                                                                                                                                                                                                                                                                                             in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; SEQ ID NO: 6925; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAH68390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-2000;
03-AUG-2000;
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 119 grefidkhdfdymiidcppslglltinamtavnevlipiqceyyalegvgql-----lnn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG93171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG93171 standard; Protein; 279
                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                    66
                                                                                                                                           58 PRIVVITSGKGGVGKTTTTANVGLSLARYGFSVVAIDADLGLRNLDLLLGLENRV-NYTC 116
                                                                                                                                                                                                           Local Similarity
                                                                                                                         7 prlitiangkggvgkttstvnlaaslaihglkvlvvdld-pqgnastalgvehrsgtlss 65
                                                                                           VEVINGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEW-----LVDAL 167
                                   KTR---PEGSPDFIIIDCPAGIDAGFITAITPANEAVLVTTPDITALRDADRVTGLLECDG
                                                                 yelligectadeam--qpstanenlfci----
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acid synthesis.
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Senoh A,
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2000JP-0280988.
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                                                                                                                                                                                                          11.9%;
26.4%;
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Ikeda
                                                                                                                                                                                           46;
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                                                                                                                                                                                                          Score 197.5; DB:
Pred. No. 3.5e-13
                                                                                                                                                                                           Mismatches
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Ozaki A;
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                                                                -patldlagaeielvslvrreyrladal 118
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                                                                                                                                                                                                                      DB 22; Length 279;
                                                                                                                                                                                           109;
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                                                                                                                                                                                          Indels
                                                                                                                                                                                          43;
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                                                                                                                                                                                        Gaps
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Вþ Qy

95

32 VNNPSRRSPIRSVLQFN-RKPELAGETP----RIVVITSGKGGVGKTTTTANVGLSLARY 86 vmsdeqrtelrkqlrgdtrepvipfaqpdsltrvyavasgkggvgkstvtvnlaaamavr 154

Matches

Similarity

11.5%;

Conservative

58;

Pred.

Score 190; DB 2 Pred. No. 4e-12; Mismatches

DB 22; 117;

Length 390; Indels

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Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ъ
                                            method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                                                  This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polypucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG811096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The
 Sequence
                                                                                                                                                                                                                                                                                                                   Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the sequences -
                                  an organism.
                                                                                                                                                                                                                                                                          Disclosure; Page 166; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH51992.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-329193/34.
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12-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2001
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 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rotstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis
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99US-0165124
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30-APR-1999; 99US-0132407. 04-MAX-1999; 99US-0132484. 05-MAY-1999; 99US-0132485. 06-MAY-1999; 99US-0132486. 06-MAY-1999; 99US-0132863. 11-MAY-1999; 99US-0134256. 14-MAY-1999; 99US-0134218. 14-MAY-1999; 99US-0134219. 14-MAY-1999; 99US-0134219. 14-MAY-1999; 99US-0134219. 14-MAY-1999; 99US-0134268. 19-MAY-1999; 99US-0134370. 18-MAY-1999; 99US-0134368. 21-MAY-1999; 99US-0134364. 21-MAY-1999; 99US-013533. 24-MAY-1999; 99US-0135629. 25-MAY-1999; 99US-0135629. 27-MAY-1999; 99US-0136021.	00000000000000000000000000000000000000	OLT 14 1.11242 AAGI1242 standard; Protein; 313 AA. AAGI1242; 17-OCT-2000 (first entry) Arabidopsis thaliana protein fragment SEQ ID NO: 9886. Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence. Arabidopsis thaliana. EP1033405-A2. 06-SEP-2000: 2000EP-0301439.	87 GESVVAIDADLGLRNLDLLLGLENRVNYTCVEVINGDCRLDOALVRDKRWSNFELLCISK 146    : :   : :  :  :  :  :  :  :  :  :  :
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21-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 26-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 28-JUL-1999 29-JUL-1999 29-JUL-1999 20-AUG-1999 01-AUG-1999 01-AUG-1999 01-AUG-1999 01-AUG-1999 01-AUG-1999	13-JUL-1999; 14-JUL-1999; 15-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999;	18 JUN 1999 21 JUN 1999 22 JUN 1999 22 JUN 1999 23 JUN 1999 24 JUN 1999 26 JUN 1999 27 JUN 1999 28 JUN 1999 29 JUN 1999 20 JUN 1999 20 JUN 1999 20 JUN 1999 20 JUN 1999 21 JUN 1999 22 JUN 1999 23 JUN 1999 26 JUN 1999 27 JUN 1999 28 JUN 1999 29 JUN 1999 20 JUN 1999	28-MAY-1999; 01-JUN-1999; 03-JUN-1999; 04-JUN-1999; 07-JUN-1999; 07-JUN-1999; 10-JUN-1999; 10-JUN-1999; 11-JUN-1999; 16-JUN-1999; 16-JUN-1999; 17-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999;
-01450 -01450 -01450 -01451 -01451 -01451 -01452 -01452 -01459 -01459 -01463 -01463 -01463	0143542 0144005 0144008 0144085 0144085 0144331 0144332 0144332 0144332 0144333 0144335 0144335 01443632	990S-0139459 990S-0139461 990S-0139461 990S-0139463 990S-0139763 990S-0139763 990S-0139879 990S-0140353 990S-0140695 990S-0140823 990S-0140823 990S-0140823 990S-0140823 990S-0141287 990S-0142803 990S-0142803 990S-0142803	0136782 0137222 01375282 0137528 0137724 0138094 0138840 0138849 0139452 0139452 0139453 0139453

04-AUG-1999; 05-AUG-1999; 05-AUG-1999; 06-AUG-1999; 06-AUG-1999;

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05-MAR 1999

09-MAR 1999

23-MAR 1999

25-MAR 1999

26-APR 1999

06-APR 1999

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54; Mismatches 88
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US-08-446-794A-2
US-08-945-44-085-1
US-08-945-20-151-4
US-08-945-024-2
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582.690 Million cell updates/sec
Patent No. 5223423
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 7, Appli
                                                                                                                                                                                                                                                                                           Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 2, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 18, Appli
                                                                                                                                                                                                                                              Sequence 18, Appl
Sequence 39, Appl
Sequence 11, Appl
Sequence 11, Appl
Patent No. 5223423
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

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STEWART, KOLASCH & BIRCH

STREET: 301 N. Washington Street CITY: Falls Church

COUNTRY:

USA

22046-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

INFORMATION FOR SEQ ID NO:

TELEFAX: /vTELEFAX: 248345

SEQUENCE CHARACTERISTICS: LENGTH: 264 amino acid

264 amino acids

TOPOLOGY: linear

amino acid

TELECOMMUNICATION INFORMATION: TELEPHONE: 703-241-1300 TELEFAX: 703-241-2848

FILING DATE: 07-FEB-1991 ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: IT M FILING DATE: 07-FEB-1991

IT MI 91A000314

APPLICATION NUMBER: US/07/661,820 FILING DATE:

NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30,330 REFERENCE/DOCKET NUMBER: 12

1267-202P

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

08/467,152

FILING DATE:

APPLICATION NUMBER: US/OFFILING DATE: 13-NOV-1997 CLASSIFICATION: 435

US/08/969,644

RESULT 1 US-08-969-644 Sequence 16 Patent No. Patent No. APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN TITLE 06 TITLE 01		45	44	43	42	41	40	39	38	37	36	35	34	ယ	32	31	30	29	28	
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16 Application US/0896964 096519 096519: Ratti, Giulio Comanducci, Maurizio Comanducci, Maurizio Comanducci, Marzia M. Invention: pcTD plasmi INVENTION: TRACHOMATIS INVENTION: TRACHOMATIS INVENTION: TRACHOMATIS		4.5	4.5	4.5	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	
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US/08969644  ulio i. Maurizio rio F. Marzia M.	ALIGNMENTS	US-08-435-434-2	US-08-282-141-2	US-08-948-176-26	5206163-3	US-08-911-321-4	US-08-583-799-6	US-08-164-839-6	US-08-583-799-4	US-08-164-839-4	US-09-413-814-3	US-09-066-047-8	US-09-306-998-3	US-09-088-435-1	US-08-439-009A-4	US-07-642-734C-4	US-08-253-155A-31	US-08-674-149A-2	US-09-461-474-15	
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Best Local Similarity
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 703-241-1300
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy
                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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     TELEFAX: /v. 248345
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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                   TELEPHONE: /UJ - 2848
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                                                                                       NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 07-FEE
                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
THEM; RECOMBINARY PLASMIDS FOR THE EXPRESSION OF SAID
GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
                                                                                                                                                                                                                       US/07/661,820
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,820
FILING DATE: 28-FEB-1991
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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LENGTH: 264 amino acids
                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                         TORNEY/AGENI INCOME.

NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330

TORNET NUMBER: 1267-202P
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                  TELEFAX:
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                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                CLASSIFICATION:
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T: 301 N. Washington Street
Falls Church
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FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08468544
                                703-241-2848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tecce, Mario F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comanducci, Maurizio
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TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED
THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
                                                                                                                                                                                                                                                                 US/08/468,544
                                                                                                                                                                 IT MI 91A000314
16:
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Pred. No. 0
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SEQUENCE CHARACTERISTICS

LENGTH:

264 amino acids

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                                                                                                  TOPOLOGY: US-08-997-445D-2
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                     Best Local
                                         Query Match
    Matches
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                                                                                                                                                                                          TELEPHONE: (617) 232-7509
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kocher, Olivier N.
TITLE OF INVENTION: PDZK1 Protein Conta
TITLE OF INVENTION: Interaction Domains
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: David Prashker
REGISTRATION NUMBER: 29,693
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 -----PDFIIIDCPAGIDAGFITAITPANEAVLVTTPDITALRDADRVTGLLE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 INGDCRLDQALVRDKRWSNFEL---LCISKPRS--KLPMGFGGKALEWLVDALKTRPEGS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 SVG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 LKLFLNEYCAPFYDICIIDTPPSLGGLTKEAFVAGDKLIACLTPEPFSILGLQKIREFLS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 --ASVRSDQKGLHDIVYTSNDLKSIICETKKDSVDLIPASFSSEQFREL--DIHRGPSNN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VVITSGKGGVGKTTTTANVGLSLARY-GFSVVAIDADLGLRNLDLLLGLENRVNYTCVEV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 5.4%; Score 88.5; DB 4; Length 264; Local Similarity 24.0%; Pred. No. 0.09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Brookline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/997,445D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LVFCSFKGGTGKTTLSLNVGCNLAQFLGKKVLLADLD-PQSNLSSGLG------ 50
                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Conservative
h 5.4%; Score 88.5; DB 3; Length 519; Similarity 19.3%; Pred. No. 0.27; 53; Conservative 38; Mismatches 76; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02146
                                                                                                                                                      amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                 December 23,
                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MS DOS
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    Indels 107;
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US-09-461-474-6
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SOFTWARE: Microsoft Office 97
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09461474 Patent No. 6278042 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               Sequence 2, Application PC/TUS9517026 GENERAL INFORMATION:
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APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1333 US NA
FILE REFERENCE: BB133 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 60/112,562
EARLIER FILING DATE: 1998-12-16
                                                            APPLICANT: USA
APPLICANT: 98102
TITLE OF INVENTION: BOV
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 TALRDADRVTGLLECDGIRDI----KMIVNRVRT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 EVSSPPDTTEEVDHKPKLCRLAKGENGYGFHLNAIRGLPGSFIKEVQKGGPA------DL 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 GDQTSLLVVDKETDNMYLRAHFSPFLYYQSQELPNG-----SVKEAPAPTPTSL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 ----QALVRDKRWSNFELLCISKP-----RSKLPMGFGGKALEWLVDALKTRPEGSPDFI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 YLRAGSEQKGQIIKDIDSGSPAEEAGLKNNDLVVA----VNGESVETLDHDSVVEMIRKG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 VDKETDKRHVEQKIQFKRETASLKLLPHQPRIVEMKKGSNG-----YGF 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 SVVA-----IDA-----DLGLRNLDLLLGLENRVNYTCVEVINGDCRLD----- 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 IVVITSGKGGVGKTTTTANVGLSLARYGFSVVAIDAD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 SLLLFS-RHQ------LRQRTL--QPHRTFRPKMSTAVISAEDALEPSLQSLLDQRSLR 61
               ADDRESSIE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                  62 WIFV-GGKGGVGKTTTSCSLAIQLAKVRRSVLLISTD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SLRLFSTNHQSLLLPSSLSQKTLISSPRFVNNPSRRSPIRS---VLQFNRKPELAGETPR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 5.3%; Score 88; DB 4; Length 376; Local Similarity 34.0%; Pred. No. 0.18; es 33; Conservative 15; Mismatches 35; Indels
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Seattle
                                                                                                                                                                                                                                       ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                  Seattle
                                                                                                                   Bovine Factor XIII
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                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08597236 Patent No. 5733765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.3%; Score 88; DB 5
Best Local_Similarity 24.2%; Pred. No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 206-442-6678 INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           470 IGGDGMKDI-----TDTYKFQEGQEEERLALETAMMYGAKKALNTEGVLKSKSDV 519
                                                                                                                                                                                                                                                                                                                                                                                                                                             224 ---DGIRDIKMIVNRVRTDMIK----GEDMMSVLDVQEMLG----LSLLGVIPEDSEV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416 QAIKHGHVCFQFDAPFVFA--EVNSDLVY----VTAKKDGTHVVEALDTTHIGKLIVTKE 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 LTKDSVW-NYH--CWNEAWMTRPDLPVGFGG----WQV--VDSTPQENSDGMYRCGPASV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 LVRDKRWSNFELLCISK----PRSKLPMGFGGKALEWLVDALKTRPEGSPDFIIIDCPAGI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 PVRYGQCWVF----AGVFNTFLRCLGIPARVVTNYFSAHDNDANLQLDIFLEEDGNVNSK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 NPIKVSRVGSAM-INAKDDEGVIAGSWDNYYAY-----GVPPSAWTGSVDILLEYKSSQK 308
                                                                                               STATE:
                                                                                                            CITY: New York
                                                               ZIP:
                                                                          COUNTRY:
                                                                                                                                   STREET:
                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 NPSRRSPIRSVLQFNRKPE---LAGETPRIVVITSGKGGVGKTTTTANVGLSL------ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31: REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------DAGFITAITPANEAVLVTTPDITALRDADRVTGLLEC------ 223
                                                           10036
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                                                                                               New York
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                                                                                                                              1155 Avenue of the Americans
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Best Local Similarity
Matches 48; Conserv
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                                                                   PRIOR APPLICATION DATA:
                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 LVIDAVIIAHQADASLLVTEAGKIKRRFVTKAVEQLVESGSQFLGVVLNKV 208
                                                                                      APPLICATION NUMBER: US/08/746,682A FILING DATE: 14-NOV-1996 CLASSIFICATION: 435
                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                            STREET:
CITY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 IDAGFITAITPANEAVLVTTPDITALRDADRVTGLLECDGIRDIKMIVNRV 236
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                APPLICATION NUMBER: 08/5 FILING DATE: 20-JUN-1995 APPLICATION NUMBER: EP 9
                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 VVAIDADLGLENLDLLLGLENRVNYTCVEVINGDCRLDQALVRDKRWSNF-----EL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/597,236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                            New York
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                                                                                                                                                                                                                                                                                           New York
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                                                                                                                                                                                                                                                                                                                           1155 Avenue of the Americans
                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 amino acids
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MOLLET, Beat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                               Pennie & Edmonds
                                                                                                                                                                                                                   Floppy disk
20-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.3%;
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                EP 95201669.9
                                                  08/597,236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SVLSGTFKSNEPY---KGLSNFLSGNADLNET 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 87; DB 1 Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                           Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
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EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1998-09-22
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                          ; ORGANISM: Streptomyces venezuelae US-09-320-878-18
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Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
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                                                   Matches
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: McDANIEL, Robert
APPLICANT: TANO, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
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TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 249 amino acid
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                                                                                                                                                                                                                                                      LENGTH: 416
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125 RLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTRPEGSPDFIIIDCPA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 LVIDAVIIAHQADASLLVTEAGKIKRRFVTKAVEQLVESGSQFLGVVLNKV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 IDAGFITAITPANEAVLYTTPDITALRDADRYTGLLECDGIRDIKMIVNRV 236
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                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 VKSKVDFAKKTEEYYNAIRTNIQFSGAQMKVIAISSVEAGEGKSMISVNLAISFASVGLR 66
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                                                   Conservative
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                                                                         5.2%; Score 86.5; DB 3; 22.2%; Pred. No. 0.31;
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                                                   31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79; Indels
                                                        73;
                                                                                                      Length 416;
                                                        Indels
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                                                        43;
                                                      Gaps
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Patent No. 6265202

GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPL
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; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-105-537-39
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Patent No. 6265202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09085199B Patent No. 6235879
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                              APPLICANT: Hayden Michael R.
APPLICANT: Hackam, Abigail
APPLICANT: Huq, A.H.M. Mahbubul
APPLICANT: Chopra, Vikramjit Singh
                                              APPLICANT: Kalchman, Michael TITLE OF INVENTION: Apoptosis Modulators That Interact with the TITLE OF INVENTION: Huntington's Disease Gene NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 RLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTRPEGSPDFIIIDCPA 184
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; Patent No. 5223423
; APPLICANT: FRANCHINI, GENOVEFFA; WONG-STAAL, FLOSSIE;
;GALLO, ROBERT
TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT;
;HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
;NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                 995 -- EAERVRLGELRKQHYVLAGGMGTPSEEEPSR 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            899 KYEELIV--CSHEI------AASTAQLVAASKVKANKNSPHLSRLQECS--RTVNER 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 GSPDFIIIDCPAGIDAGFITAITPANEAVLYTTPDITALRDADRVTGLLECDGIRDIKMI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 AFEQAAWRLVEQDSMKAVMV-----EEEPKK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                946 AANVVASTKSGQEQIEDRDTMDFSGLSLIKLKKQEMETQVR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 VNRVRTDMIKGEDMMSVLDVQEMLGLSLLGVIPEDSEV-IRSTNRGFPLVLNKPPTLAGL 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 NYTCVEVINGDCRLDQALVRDKRWSNFELLCISKPRSKLPMGFGGKALEWLVDALKTRPE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  787 MAATS--AAIEDAVRRIEDMMSQARHESSGVKLEVNERILNSCTDLMKAIRLLVMTSTSL 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731 RALELVGQLQDQTVLRRAQ----PSLMRAPLQGILQLGQDLKPKSLDVRQEELGAMVDKE 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDITE FOR STREET: FC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y match
Local Similarity 20.7%; pred. No. 1.9;
les 69; Conservative 52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 QSLLLPSSLSQKTLISSPRFVNNPS-RRSPIRSVLQFN------RKPELAGETPRI 60
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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US-08-416-603-4
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US-08-416-603-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                          TELEPHONE: 904-375-8100 INFORMATION FOR SEQ ID NO: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hebara, L
APPLICANT: Reddick,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeffrey
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                MOLECULE TYPE:
                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA
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APPLICATION NUMBER: US,
FILING DATE: 03-31-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2248 FHSQKIINKKPRQAWCRF-KGEWREAMQE-VKQTLV-KHPRYKG 2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2145 AMRERYCAPPGEVLLRCNDTNYSGE----EPNCSKVVAST--CTRMMETQPSTWL----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2094 LE-----LDKKKQYSETWYSKDVVCESDNSTDRKRCYMNHCNTSVITESCDKHYW--D 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2037 TPLCVTMNCNASTESAVATTSPSGPDMINDTDPCIQLNNCSGLREEDM----VECQFNMTG 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 F--PLVLNKPPTLAGLAFEQAAWRLVEQDSMKAVMVEEEPKKRG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 IRDIKMIVNRVRTD-----MIKGEDMMSVLDVQEMLGLSLLGVIPEDSEVIRST---NRG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 ALKTRPEGSPDFIIIDCPAGIDAGFITAITPANEAVLVTTPDITALRDADRVTGLLECDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 VEVINGDCRLDQALVRDKRWSNFELLC---ISKPRSKLPMGFGGKAL-----EWLVD 165
                                  TYPE: amino acid TOPOLOGY: linear
                                                    TYPE:
                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                      LENGTH:
                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3077
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gainesville
: FL
                                                                      3457 amino acids
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2421 N.W. 41st Street, Suite
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Reddick, Bradford B.
VENTION: Maize Chlorotic Dwarf Virus Genome and
VENTION: Uses Therefor
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21.5%; Pred. No. 17;
                                                                                                                                                                                                                                                                  US/08/416,603
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                                                                                                                                                                     35,589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suite A-1
                                                                                                                                                                                                                                                                                                      Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3077;
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US-08-896-320-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,320
FILING DATE: Herewith
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2987 QS----DYWQQIEMDTSSGWPYAKRKPVGAAGK--KWLFEQDGTYPSGKPRYVFGD--AG 3038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2933 VIEASM---KYGSRITPFPVDQILEVEDHLSKMLANCENSKNKRQVNNLEIGING---ID 2986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purt
TITLE OF INVENTION: HUMAN DEVELOPMENTALLY REGULATED
TITLE OF INVENTION: GTP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,7
REFERENCE/DOCKET NUMBER:
                                                                                                                             SEQUENCE CHARACTERISTICS LENGTH: 367 amino aci
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                   IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 QALVRDKRWSNFELLCISK-PRSK-LPMGFGGKALEWLVDALKTRPEGSPDFIIIDCPAG 185
     MELLE CALL
LIBRARY: CALL
TONE: 281964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 TANVGLSLARYGFSVVAIDADLGLRNLD----LLLGLENRVNYTCV---EV-INGDCRLD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 SSLSQKTLISSPRFVNNPSRRSPIRSVL-QENRKPE-LAGETPRIVVITSGKGGVGKTTT 75
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                                                                                       STRANDEDNESS:
                                                                                                               TYPE:
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                                                                                                             amino acid
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                                                                                                                             367 amino acids
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                                     CARDNOT01
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                                                                       linear
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                                                                                         single
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25.1%; Pred. No. 21;
                                                                                                                                                                                                                                                                                36,749
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                                                                                     US-08-896-320-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08896320 Patent No. 5871971
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Best Local Similarity
Matches
                              Query Match
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                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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APPLICANT: Lal, p
APPLICANT: Corley
APPLICANT: Shah,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                    IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 220507
                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 RWSNFELLCISKPRSKLPMGFGGKALEWLVDALK-----TRPEGS-PDF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 IRLNSKP-----PNIGFKKKDKGGINLTATCPQSELDAETVKSILAEYKIH----NADV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 TLRSDATADDLIDVVEG--NRVYIPCIYVLN---KIDQISIEELDIIYKVPHCVPISAHH 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 GLRN------KDLLLGLENRVNYTCVEVINGDCRLDQALVRD------K 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
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               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                TELEFAX; 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                           amino acid
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Shah, Purvi
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Conservative
                                                                                                                         GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                           linear
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             5.0%; Score 82.5; DB 2; 25.4%; Pred. No. 0.73;
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20;
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Mismatches
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 37;
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                                  Length 367;
 Indels
 69; Gaps
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45 LQFNRKPELAGETPRIVVITSGKGGVGKTTTTANVGLS-----LARYGFSVVAIDADL 97

Db	Qy	DЪ	Qy	Db
275 RW-NFDDLLEKIWDYLKLVRIYTKPKGQLPDY 305	ISKPRSKLPMGF	220 TLRSDATADDLIDVVEGNRVYIPCIYVLNKIDQISIEELDIIYKVPHCVPISAHH 274	98 GLRNK 134	::      :  :  :  :  :  :  :  :  :  :  :
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Search completed: February 11, 2002, 13:31:36 Job time: 23 sec